

Minnifield
10/789536

10/789536

L1 FILE 'REGISTRY' ENTERED AT 12:10:19 ON 21 JAN 2005
157 S GGGGTCAACGTTTCAGGGGGG | GCATGACGTTGAGCT/SQSN

L2 FILE 'CAPLUS' ENTERED AT 12:12:01 ON 21 JAN 2005
55 S L1

L8 21 SEA ABB=ON PLU=ON L2(L) (IMMUNOMODULAT? OR IMMUNOSTIMULAT? OR
IMMUNOSTIMULANT OR IMMUNORESPONS? OR (IMMUN# OR IMMUNOL?) (3A) (M
ODULAT? OR STIMULAT? OR STIMULANT OR RESPONS?))

E1 THROUGH E29 ASSIGNED

Searcher : Shears 571-272-2528

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 01:27:37 ; Search time 588 Seconds

(without alignments)
1608.493 Million cell updates/sec

Title: US-10-789-536-1
Perfect score: 20
Sequence: 1 GGGGTCACGCTCAGG9999 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_da.*
2: gb_hg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pac.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_st.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	20	100.0	20 6 AR096686	AR096686 Sequence
2	20	100.0	20 6 AR135030	AR135030 Sequence
3	20	100.0	20 6 AX342378	AX342378 Sequence
4	20	100.0	20 6 AX342405	AX342405 Sequence
5	20	100.0	20 6 AX342438	AX342438 Sequence
6	20	100.0	20 6 AR140453	AR140453 Sequence
7	20	100.0	20 6 AR154761	AR154761 Sequence
8	20	100.0	20 6 BD190419	BD190419 Microemul
9	20	100.0	20 6 BD251267	BD251267 Enhanceme
10	20	100.0	20 6 AR182880	AR182880 Sequence
11	20	100.0	20 6 AR182887	AR182887 Sequence
12	20	100.0	20 6 AR222213	AR222213 Sequence
13	20	100.0	20 6 AR432435	AR432435 Sequence
14	20	100.0	20 6 AX063578	AX063578 Sequence
15	20	100.0	20 6 AX088932	AX088932 Sequence
16	20	100.0	20 6 AX104327	AX104327 Sequence
17	20	100.0	20 6 AX104575	AX104575 Sequence
18	20	100.0	20 6 AX104776	AX104776 Sequence
19	20	100.0	20 6 AX104777	AX104777 Sequence

Result	Score	Query Match	Best Local Similarity	Matches	20; Conservative	0; Mismatches	Score 20; DB 6; Length 20; Pred. No. 19; 0; Indels 0; Gaps 0;
20	18.4	92.0	20 6 AX105103	AX105103 Sequence			
21	18.4	92.0	20 6 AX105236	AX105236 Sequence			
22	18.4	92.0	20 6 AX135634	AX135634 Sequence			
23	18.4	92.0	20 6 AX194489	AX194489 Sequence			
24	18.4	92.0	20 6 AX355408	AX355408 Sequence			
25	18.4	92.0	20 6 AX355409	AX355409 Sequence			
26	18.4	92.0	20 6 AX465439	AX465439 Sequence			
27	18.4	92.0	20 6 AX468483	AX468483 Sequence			
28	18.4	92.0	20 6 AX547380	AX547380 Sequence			
29	18.4	92.0	20 6 AX547628	AX547628 Sequence			
30	18.4	92.0	20 6 AX547829	AX547829 Sequence			
31	18.4	92.0	20 6 AX547830	AX547830 Sequence			
32	18.4	92.0	20 6 BD009060	BD009060 Immunobrl			
33	18.4	92.0	20 6 BD069974	BD069974 Use of nu			
34	18.4	92.0	21 6 AX104812	AX104812 Sequence			
35	18.4	92.0	21 6 AX105257	AX105257 Sequence			
36	18.4	92.0	21 6 AX547865	AX547865 Sequence			
37	18.4	92.0	24 6 AX104326	AX104326 Sequence			
38	18.4	92.0	24 6 AX547379	AX547379 Sequence			
39	17.4	87.0	19 6 CO753472	CO753472 Sequence			
40	17.4	87.0	19 6 CO753473	CO753473 Sequence			
41	17.4	87.0	19 6 AX194446	AX194446 Sequence			
42	17.4	87.0	19 6 AX465396	AX465396 Sequence			
43	17.4	87.0	19 6 AX771751	AX771751 Sequence			
44	17.4	87.0	19 6 AX771752	AX771752 Sequence			
45	17.4	87.0	2 AC013515	AC013515 Homo sapi			

ALIGNMENTS

RESULT 1
LOCUS AR096686 20 bp DNA
DEFINITION Sequence 1 from patent US 6008200.
ACCESSION AR096686
VERSION AR096686.1 GI:10025701
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 20)
TITLE Immunomodulatory oligonucleotides
JOURNAL Patent: US 6008200-A 1-28-DEC-1999;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTCACGCTCAGG9999 20
Db 1 GGGGTCACGCTCAGG9999 20

RESULT 2
LOCUS AR135030 20 bp DNA
DEFINITION Sequence 1 from patent US 6194388.
ACCESSION AR135030
VERSION AR135030.1 GI:14123935
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 20)
TITLE Immunomodulatory oligonucleotides

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 05:57:22 (Search time 48 Seconds
(without alignments)
296.162 Million cell updates/sec

Title: US-10-789-536-1

Sequence: 1 99595caccgttcagggg995 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
4: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
5: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
6: /cgn2_6/prodata/1/ina/5B_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-08-386-063-1
2	20	100.0	20	3	US-08-386-063-1
3	18.4	92.0	20	3	US-08-386-063-1
4	18.4	92.0	20	3	US-08-386-063-1
5	18.4	92.0	20	3	US-08-386-063-1
6	18.4	92.0	20	3	US-08-386-063-1
7	18.4	92.0	20	3	US-08-386-063-1
8	18.4	92.0	20	3	US-08-386-063-1
9	18.4	92.0	20	3	US-08-386-063-1
10	18.4	92.0	20	3	US-08-386-063-1
11	18.4	92.0	20	3	US-08-386-063-1
12	18.4	92.0	20	3	US-08-386-063-1
13	18.4	92.0	20	3	US-08-386-063-1
14	18.4	92.0	20	3	US-08-386-063-1
15	18.4	92.0	20	3	US-08-386-063-1
16	18.4	92.0	20	3	US-08-386-063-1
17	18.4	92.0	20	3	US-08-386-063-1
18	18.4	92.0	20	3	US-08-386-063-1
19	18.4	92.0	20	3	US-08-386-063-1
20	18.4	92.0	20	3	US-08-386-063-1
21	18.4	92.0	20	3	US-08-386-063-1
22	18.4	92.0	20	3	US-08-386-063-1
23	18.4	92.0	20	3	US-08-386-063-1
24	18.4	92.0	20	3	US-08-386-063-1
25	18.4	92.0	20	3	US-08-386-063-1
26	18.4	92.0	20	3	US-08-386-063-1
27	18.4	92.0	20	3	US-08-386-063-1

28	14.8	74.0	1554	4	US-09-270-767-11891	Sequence 11891, A
29	14.8	74.0	30350	4	US-10-118-328-3	Sequence 3, App1
30	14.8	74.0	50341	2	US-08-247-901C-1	Sequence 1, App1
31	14.8	74.0	50341	2	US-09-075-904-1	Sequence 1, App1
32	14.8	74.0	52297	3	US-09-426-436-1	Sequence 1, App1
33	14.8	74.0	52297	3	US-08-705-557-1	Sequence 1, App1
34	14.4	72.0	318	4	US-08-150-204E-97	Sequence 97, App1
35	14.4	72.0	318	4	US-08-150-204E-104	Sequence 104, App
36	14.4	72.0	318	4	US-08-150-204E-106	Sequence 106, App
37	14.4	72.0	318	4	US-08-150-204E-110	Sequence 110, App
38	14.4	72.0	318	4	US-08-150-204E-112	Sequence 112, App
39	14.4	72.0	318	4	US-08-150-204E-119	Sequence 119, App
40	14.4	72.0	1426	4	US-09-464-535-41	Sequence 41, App1
41	14.4	72.0	3780	4	US-09-489-039A-1669	Sequence 1669, App
42	14.4	72.0	8637	4	US-09-539-601-4	Sequence 4, App1
43	14.4	72.0	8638	4	US-10-029-907-6	Sequence 6, App1
44	14.4	72.0	8638	4	US-10-029-907-7	Sequence 7, App1
45	14.4	72.0	8638	4	US-10-029-907-24	Sequence 24, App1

ALIGNMENTS

RESULT 1
US-08-386-063-1
Sequence 1, Application US/08386063
Patent No. 6008200
GENERAL INFORMATION:
APPLICANT: Arthur M. Krieg, M.D.
TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/386,063
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ARNOLD, BETH E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIZ-013CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-386-063-1
Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GGGGTCACGTTACGGGGG 20
DB 1 GGGGTCACGTTACGGGGG 20
RESULT 2

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OM nucleic - nucleic search, using SW model

Run on: January 19, 2005, 06:37:10 ; Search time 209.714 Seconds
(without alignments)
547.973 Million cell updates/sec

Title: US-10-789-536-1

Perfect score: 20
1 9999TCAAGTCAAG9999 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	10	US-09-415-142-1
2	20	100.0	20	10	US-09-931-583-1
3	20	100.0	20	16	US-10-631-676-1
4	20	100.0	20	17	US-10-789-051-1
5	20	100.0	20	17	US-10-680-495-1
6	20	100.0	20	17	US-10-788-191-1
7	20	100.0	20	17	US-10-789-536-1
8	20	100.0	20	17	US-10-769-626-1
9	20	100.0	20	17	US-10-789-353-1
10	20	100.0	20	17	US-10-787-737-1
11	20	100.0	20	17	US-10-788-199-1
12	20	100.0	20	18	US-10-847-650-1

13	18.4	92.0	20	10	US-09-888-326-436	Sequence 436, App
14	18.4	92.0	20	10	US-09-888-326-437	Sequence 437, App
15	18.4	92.0	20	10	US-09-818-918-12	Sequence 12, App1
16	18.4	92.0	20	10	US-09-776-479-519	Sequence 519, App
17	18.4	92.0	20	10	US-09-776-479-519	Sequence 767, App
18	18.4	92.0	20	10	US-09-776-479-968	Sequence 968, App
19	18.4	92.0	20	10	US-09-776-479-969	Sequence 969, App
20	18.4	92.0	20	10	US-09-967-664-3	Sequence 3, App1
21	18.4	92.0	20	11	US-09-776-479-519	Sequence 519, App
22	18.4	92.0	20	11	US-09-776-479-519	Sequence 767, App
23	18.4	92.0	20	11	US-09-776-479-968	Sequence 968, App
24	18.4	92.0	20	11	US-09-776-479-969	Sequence 969, App
25	18.4	92.0	20	11	US-09-965-101-52	Sequence 52, App1
26	18.4	92.0	20	11	US-09-965-101-59	Sequence 59, App1
27	18.4	92.0	20	14	US-10-112-653-496	Sequence 496, App
28	18.4	92.0	20	14	US-10-112-653-740	Sequence 740, App
29	18.4	92.0	20	14	US-10-112-653-923	Sequence 923, App
30	18.4	92.0	20	14	US-10-017-995-519	Sequence 519, App
31	18.4	92.0	20	14	US-10-017-995-767	Sequence 767, App
32	18.4	92.0	20	14	US-10-017-995-968	Sequence 968, App
33	18.4	92.0	20	14	US-10-017-995-969	Sequence 969, App
34	18.4	92.0	20	15	US-10-161-229-47	Sequence 47, App1
35	18.4	92.0	20	15	US-10-194-035-89	Sequence 89, App1
36	18.4	92.0	20	15	US-10-224-523-35	Sequence 35, App1
37	18.4	92.0	20	15	US-10-187-264A-12	Sequence 12, App1
38	18.4	92.0	20	15	US-10-306-522-12	Sequence 12, App1
39	18.4	92.0	20	15	US-10-314-578-519	Sequence 519, App
40	18.4	92.0	20	15	US-10-314-578-767	Sequence 767, App
41	18.4	92.0	20	15	US-10-314-578-968	Sequence 968, App
42	18.4	92.0	20	15	US-10-314-578-969	Sequence 969, App
43	18.4	92.0	20	16	US-10-455-247-3	Sequence 3, App1
44	18.4	92.0	20	16	US-10-719-493-12	Sequence 12, App1
45	18.4	92.0	20	17	US-10-627-331-12	Sequence 12, App1

ALIGNMENTS

RESULT 1
US-09-415-142-1
Sequence 1, Application US/09415142
Publication No. US20030026782A1
GENERAL INFORMATION:
APPLICANT: Kline, Arthur M.
APPLICANT: Kline, Dennis
TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
FILE REFERENCE: C1039/7029
CURRENT APPLICATION NUMBER: US/09/415,142
CURRENT FILING DATE: 1999-10-09
PRIORITY APPLICATION NUMBER: US 08/386,063
PRIORITY FILING DATE: 1995-02-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
US-09-415-142-1

Query Match 100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTCAACGTTACAGGGG 20
Db 1 GGGGTCAACGTTACAGGGG 20

RESULT 2
US-09-931-583-1

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: January 19, 2005, 05:49:12 ; Search time 1626.29 Seconds
(without alignments)
448.134 Million cell updates/sec

Title: US-10-789-536-1

Perfect score: 20

Sequence: 1 999gtcaacgtcagcagcagcagc 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_g881: *
9: gb_g882: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.4	92.0	414	5	BX678404 BX678404
2	18.4	92.0	558	5	BX253788 BX253788
3	17.4	87.0	281	1	AV294749 AV294749
4	17.4	87.0	437	1	AV772436 AV772436
5	17.4	87.0	692	9	CG143495 PUIH657B
6	17.4	87.0	708	2	BB629098 BB629098
7	17.4	87.0	721	8	AQ414593 RPCI-11-1
8	17.4	87.0	884	8	BH950547 od13c04
9	16.8	84.0	223	7	CF398170 RTD33_21
10	16.8	84.0	243	2	BE643702 NCX1_043
11	16.8	84.0	336	2	BB532888 BB532888
12	16.8	84.0	341	2	AM888010 NXNV_105
13	16.8	84.0	381	5	BF516817 NXSI_003
14	16.8	84.0	388	5	BQ701308 NXSI_062
15	16.8	84.0	395	2	BX678528 BX678528
16	16.8	84.0	395	6	CD028242 NXNV004A0
17	16.8	84.0	451	2	BE831401 NXNV_181
18	16.8	84.0	451	2	BE831401 NXNV_181
19	16.8	84.0	477	5	BQ655830 NXRV099_H
20	16.8	84.0	492	5	BQ700582 NXRV108_B
21	16.8	84.0	495	7	CF392169 RTDR3_8_B
22	16.8	84.0	505	1	A1813183 23H_Pine
23	16.8	84.0	505	2	AM985091 NXNV_130
24	16.8	84.0	505	2	AM985091 NXNV_130

C 25	16.8	84.0	512	2	BF517774	BF517774 NXSI_031
C 26	16.8	84.0	530	6	CA354197	CA354197 625871_NC
C 27	16.8	84.0	532	4	BC275515	BC275515 NXSI_139
C 28	16.8	84.0	546	1	AA556997	AA556997 839_Lob10
C 29	16.8	84.0	561	7	CF673102	CF673102 RTCN1_76
C 30	16.8	84.0	566	7	CF476621	CF476621 RTW3_2_D
C 31	16.8	84.0	598	7	CF392026	CF392026 RTDR3_12
C 32	16.8	84.0	626	1	AL751023	AL751023 AL751023
C 33	16.8	84.0	626	1	AA557077	AA557077 919_Lob10
C 34	16.8	84.0	634	5	BX253042	BX253042 BX253042
C 35	16.8	84.0	641	5	BX784262	BX784262 BX784262
C 36	16.8	84.0	648	7	CF389798	CF389798 RTDR2_5_E
C 37	16.8	84.0	653	5	BO633853	BO633853 NXRV061_P
C 38	16.8	84.0	660	7	CF401770	CF401770 RTW1_14
C 39	16.8	84.0	662	7	CF386290	CF386290 RTDR1_13
C 40	16.8	84.0	662	7	CF390498	CF390498 RTDR2_19
C 41	16.8	84.0	666	7	CO199154	CO199154 GEO1_19_E
C 42	16.8	84.0	676	7	CF670509	CF670509 RTCN1_50
C 43	16.8	84.0	691	7	CF473420	CF473420 RTW2_2_A
C 44	16.8	84.0	694	7	CO174200	CO174200 ND1_42_A
C 45	16.8	84.0	700	8	AO888815	AO888815 HS_3144_A

ALIGNMENTS

RESULT 1
BX678404/C
LOCUS BX678404 414 bp mRNA linear EST 28-OCT-2003
DEFINITION BX678404 RS Pinus pinaster CDNA clone RS08F09, mRNA sequence.
ACCESSION BX678404
VERSION BX678404.1 GI:38012342
KEYWORDS EST.
SOURCE Pinus pinaster
ORGANISM Pinus pinaster
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE 1 (bases 1 to 414)
Frigerio, J. and Plomion, C.
Identification of water-deficit responsive genes in Maritime pine
(Pinus pinaster Ait.) using an EST approach
Unpublished (2002)
JOURNAL
Contact: Frigerio JM
COMMENT
Genetique et Amelioration 69
INRA
route d'Arcachon 33612 Cestas CEDEX France
Email: Frigerio@piereton.inra.fr
Email: Frigerio@piereton.inra.fr
Seq primer: T3.

FEATURES

source
Location/Qualifiers
1..414
/organism="Pinus pinaster"
/mol_type="mRNA"
/db_xref="taxon:71647"
/clone="RS08F09"
/tissue_type="root"
/dev_stage="6 weeks old seedling"
/lab_host="SOLR"
/note="Vector: Uni-ZAP XR; ecotype: Landes; The library was made from the roots of 6 weeks old seedlings grown in hydroponic conditions. A three weeks drought stress treatment was applied by lowering the osmotic potential of the nutrient solution to -0.45 MPa using 170 g/l of polyethylene glycol as an osmoticum. A mixture of genotypes were used. Oligo-dr primed cDNA was directionally cloned into the EcoRI-XhoI lambda-ZAP vector arms and mass-excised to form a plasmid phageid"

ORIGIN

Query Match 92.0%; Score 18.4; DB 5; Length 414;
Best Local Similarity 95.0%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using SW model

Run on: January 19, 2005, 01:27:37 ; Search time 441 Seconds

(without alignments)
1608.493 Million cell updates/sec

Title: US-10-789-536-6

Sequence: 1 gcatacgttgagct 15

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 2364849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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2: gb_hcg:*
3: gb_in:*
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5: gb_ov:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_ets:*
12: gb_gy:*
13: gb_un:*
14: gb_vt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	15	6 AR096691	AR096691 Sequence
2	15	100.0	15	6 AR135035	AR135035 Sequence
3	15	100.0	15	6 AR140447	AR140447 Sequence
4	15	100.0	15	6 AR140457	AR140457 Sequence
5	15	100.0	15	6 AR140489	AR140489 Sequence
6	15	100.0	15	6 AR146293	AR146293 Sequence
7	15	100.0	15	6 AR146329	AR146329 Sequence
8	15	100.0	15	6 AR154677	AR154677 Sequence
9	15	100.0	15	6 BD205515	BD205515 Sequence
10	15	100.0	15	6 BD205551	BD205551 Method of
11	15	100.0	15	6 BD261057	BD261057 Method of
12	15	100.0	15	6 BD261093	BD261093 Method a
13	15	100.0	15	6 BD261226	BD261226 Method a
14	15	100.0	15	6 BD267831	BD267831 Method a
15	15	100.0	15	6 BD267861	BD267861 Method f
16	15	100.0	15	6 BD270732	BD270732 Stereoiso
17	15	100.0	15	6 AR213813	AR213813 Sequence
18	15	100.0	15	6 AR222180	AR222180 Sequence
19	15	100.0	15	6 AR432429	AR432429 Sequence

20	15	100.0	15	6 AX103874	AX103874 Sequence
21	15	100.0	15	6 AX103894	AX103894 Sequence
22	15	100.0	15	6 AX104574	AX104574 Sequence
23	15	100.0	15	6 AX104591	AX104591 Sequence
24	15	100.0	15	6 AX104643	AX104643 Sequence
25	15	100.0	15	6 AX105164	AX105164 Sequence
26	15	100.0	15	6 AX105183	AX105183 Sequence
27	15	100.0	15	6 AX105184	AX105184 Sequence
28	15	100.0	15	6 AX342410	AX342410 Sequence
29	15	100.0	15	6 AX342443	AX342443 Sequence
30	15	100.0	15	6 AX351733	AX351733 Sequence
31	15	100.0	15	6 AX351799	AX351799 Sequence
32	15	100.0	15	6 AX351820	AX351820 Sequence
33	15	100.0	15	6 AX351844	AX351844 Sequence
34	15	100.0	15	6 AX351871	AX351871 Sequence
35	15	100.0	15	6 AX351892	AX351892 Sequence
36	15	100.0	15	6 AX352112	AX352112 Sequence
37	15	100.0	15	6 AX352131	AX352131 Sequence
38	15	100.0	15	6 AX355037	AX355037 Sequence
39	15	100.0	15	6 AX355291	AX355291 Sequence
40	15	100.0	15	6 AX355292	AX355292 Sequence
41	15	100.0	15	6 AX355293	AX355293 Sequence
42	15	100.0	15	6 AX355294	AX355294 Sequence
43	15	100.0	15	6 AX455576	AX455576 Sequence
44	15	100.0	15	6 AX546927	AX546927 Sequence
45	15	100.0	15	6 AX546947	AX546947 Sequence
			6	AX547627	AX547627 Sequence

ALIGNMENTS

RESULT 1
LOCUS AR096691 15 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 6 from patent US 6008200.
ACCESSION AR096691
VERSION AR096691.1 GI:10025709
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 15)
TITLE Kriegl,A.M.
JOURNAL Immunomodulatory oligonucleotides
FEATURES Patent: US 6008200-A 6-28-DEC-1999;
Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GCATGACGTTGAGCT 15
Db 1 GCATGACGTTGAGCT 15

RESULT 2
LOCUS AR135035 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 6 from patent US 6194388.
ACCESSION AR135035
VERSION AR135035.1 GI:14123940
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 15)
TITLE Kriegl,A.M.; Kilman,D. and Steinberg,A.D.
Immunomodulatory oligonucleotides

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OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 01:18:22 ; Search time 148.286 Seconds
(without alignments)
531.011 Million cell updates/sec

Title: US-10-789-536-6

Sequence: 1 gcatgacgtctgacct 15

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N GeneSeq 23Sep04:*

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- 2: geneSeq1990s:*
- 3: geneSeq2000s:*
- 4: geneSeq2001as:*
- 5: geneSeq2001bs:*
- 6: geneSeq2002as:*
- 7: geneSeq2002bs:*
- 8: geneSeq2003as:*
- 9: geneSeq2003bs:*
- 10: geneSeq2003cs:*
- 11: geneSeq2003ds:*
- 12: geneSeq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	15	100.0	15	2	AAV52553 Unmethy1a
2	15	100.0	15	2	AAV27727 Immunost1
3	15	100.0	15	2	AAV27673 Immunost1
4	15	100.0	15	2	AAV27679 Immunost1
5	15	100.0	15	2	AAV27712 Immunost1
6	15	100.0	15	2	AAV27712 Immunost1
7	15	100.0	15	2	AAZ41860 IL-12 sec
8	15	100.0	15	3	AAZ41860 IL-12 sec
9	15	100.0	15	3	AAZ47936 Immune re
10	15	100.0	15	3	AAZ47936 Immune re
11	15	100.0	15	3	AAZ47936 Immune re
12	15	100.0	15	3	AAZ47936 Immune re
13	15	100.0	15	3	AAZ48839 B-cell st
14	15	100.0	15	3	AAZ47628 Parasitic
15	15	100.0	15	4	AAH50576 Murine IL
16	15	100.0	15	4	AAH19256 Phosphoro
17	15	100.0	15	4	AAH19266 Cpg Oligo
18	15	100.0	15	4	AAH19298 Cpg Oligo
19	15	100.0	15	4	AAH19298 Cpg Oligo
20	15	100.0	15	4	AAH19298 Cpg Oligo
21	15	100.0	15	4	AAH78645 Nucleotid

22	15	100.0	15	4	AAH99583	AAH99583 Immunost1
23	15	100.0	15	4	AAH99566	AAH99566 Immunost1
24	15	100.0	15	4	AAH99630	AAH99630 Immunost1
25	15	100.0	15	4	AAH99841	AAH99841 Immunost1
26	15	100.0	15	4	AAH99861	AAH99861 Immunost1
27	15	100.0	15	4	AAH78474	AAH78474 Nucleotid
28	15	100.0	15	6	ABL35122	ABL35122 Immunost1
29	15	100.0	15	6	ABL35485	ABL35485 Immunost1
30	15	100.0	15	6	ABL35186	ABL35186 Immunost1
31	15	100.0	15	6	ABL35502	ABL35502 Immunost1
32	15	100.0	15	6	ABL35205	ABL35205 Immunost1
33	15	100.0	15	6	ABL35252	ABL35252 Immunost1
34	15	100.0	15	6	ABL35228	ABL35228 Immunost1
35	15	100.0	15	6	ABL35271	ABL35271 Immunost1
36	15	100.0	15	6	ABH77582	ABH77582 Angiogene
37	15	100.0	15	6	ABH77299	ABH77299 Angiogene
38	15	100.0	15	6	ABH77602	ABH77602 Angiogene
39	15	100.0	15	6	ABH78351	ABH78351 Angiogene
40	15	100.0	15	6	ABH78282	ABH78282 Angiogene
41	15	100.0	15	6	ABL38922	ABL38922 Immunost1
42	15	100.0	15	6	ABL38702	ABL38702 Immunost1
43	15	100.0	15	6	ABL38923	ABL38923 Immunost1
44	15	100.0	15	6	ABL38921	ABL38921 Immunost1
45	15	100.0	15	6	ABL38920	ABL38920 Immunost1

ALIGNMENTS

RESULT 1

AAV52553 standard; DNA; 15 BP.

AAV52553;

20-NOV-1998 (first entry)

Unmethylated Cpg dinucleotide 1823.

Unmethylated Cpg dinucleotide; immune response; bacterial meningitis;
natural killer cell activation; NK cell; Th2 response; neonatal sepsis;
pulmonary disorder; asthma; environmentally induced airway disease;
bacterial infection; endotoxaemia; therapy; cystic fibrosis;
inflammatory bowel disease; ss.

Synthetic.

WO9837919-A1.

03-SEP-1998.

25-FEB-1998; 98WO-US003678.

28-FEB-1997; 97US-0039405P.

(IOWA) UNIV IOWA RES FOUND.

Schwartz DA, Krieg AM;

WPI; 1998-480941/41.

Use of nucleic acids containing an unmethylated Cpg - for treating a
subject having or at risk of having an acute decrement in air flow or
inhibiting an inflammatory response.

Example 4; Page 35; 65pp; English.

This sequence represents an unmethylated Cpg dinucleotide, and can be
used in the method of the invention. The method is for treating a subje
ct having, or at risk of having an acute decrement in air flow, comprising
administering a nucleic acid sequence containing at least one
unmethylated Cpg. The nucleic acid sequence containing an unmethylated Cpg
dinucleotide affect an immune response in a subject by activating natural

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OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 05:57:22 | Search time 36 Seconds
(without alignments)
296.162 Million cell updates/sec

Title: US-10-789-536-6
Perfect score: 15
Sequence: 1 gcacgacgttgagct 15

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents, NA:
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2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	15	US-08-386-063-6	Sequence 6, Appli
2	15	100.0	15	US-08-386-063-6	Sequence 6, Appli
3	15	100.0	15	US-08-738-652-6	Sequence 16, Appli
4	15	100.0	15	US-08-738-652-16	Sequence 48, Appli
5	15	100.0	15	US-08-738-652-48	Sequence 35, Appli
6	15	100.0	15	US-09-030-701-35	Sequence 5, Appli
7	15	100.0	15	US-09-286-098-5	Sequence 41, Appli
8	15	100.0	15	US-09-286-098-41	Sequence 6, Appli
9	15	100.0	15	US-09-960-774-6	Sequence 5, Appli
10	15	100.0	15	US-09-325-193A-5	Sequence 5, Appli
11	15	100.0	15	US-09-191-170-5	Sequence 6, Appli
12	15	100.0	15	US-09-337-619-6	Sequence 1544, Ap
13	15	89.3	519	US-09-543-681A-1544	Sequence 1598, Ap
14	15	89.3	522	US-09-543-681A-1598	Sequence 261, App
15	15	89.3	999	US-09-489-039A-261	Sequence 261, App
16	15	89.3	1001	US-09-641-638-261	Sequence 1840, Ap
17	15	89.3	1001	US-10-170-097-261	Sequence 33, Appli
18	15	89.3	1842	US-09-543-681A-1840	Sequence 675, App
19	15	89.3	1896	US-08-426-630-33	Sequence 3, Appli
20	15	89.3	2935	US-09-620-312D-676	Sequence 3, Appli
21	15	89.3	3039	US-09-620-312D-675	Sequence 3, Appli
22	15	89.3	3808	US-08-916-917-3	Sequence 3, Appli
23	15	89.3	3808	US-08-972-631-3	Sequence 3, Appli
24	15	89.3	3808	US-08-972-628-3	Sequence 3, Appli
25	15	89.3	3808	US-08-972-630-3	Sequence 3, Appli
26	15	89.3	3808	US-08-672-211-3	Sequence 3, Appli
27	15	89.3	3808	US-09-225-170-3	Sequence 3, Appli

C	28	13.4	89.3	4748	4	US-08-426-630-29	Sequence 29, Appli
C	29	13.4	89.3	6045	4	US-09-091-501B-7	Sequence 7, Appli
C	30	13.4	89.3	10320	4	US-09-091-501B-9	Sequence 9, Appli
C	31	13.4	89.3	111282	3	US-09-754-250-3	Sequence 3, Appli
C	32	13	86.7	343	3	US-08-349-403-7	Sequence 7, Appli
C	33	13	86.7	528	4	US-09-248-796A-3977	Sequence 3977, Ap
C	34	13	86.7	1089	4	US-09-489-039A-2302	Sequence 2302, Ap
C	35	13	86.7	1179	4	US-09-603-787A-185	Sequence 185, App
C	36	13	86.7	1551	1	US-08-457-274A-1	Sequence 1, Appli
C	37	13	86.7	1551	1	US-08-457-274A-27	Sequence 27, Appli
C	38	13	86.7	1551	5	PCT-US95-05758-1	Sequence 1, Appli
C	39	13	86.7	1551	5	PCT-US95-05758-27	Sequence 27, Appli
C	40	13	86.7	2046	4	US-09-489-039A-4692	Sequence 4692, Ap
C	41	13	86.7	2085	1	US-08-457-274A-29	Sequence 29, Appli
C	42	13	86.7	2085	5	PCT-US95-05758-29	Sequence 29, Appli
C	43	13	86.7	2435	4	US-09-634-238-131	Sequence 131, App
C	44	13	86.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
C	45	13	86.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-386-063-6
Sequence 6, Application US/08386063
Patent No. 6086200
GENERAL INFORMATION:
APPLICANT: Arthur M. Krieg, M.D.
TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/386,063
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ARNOLD, BETH E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIZ-013CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-386-063-6

Query Match 100.0%; Score 15; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GCATGACGTGAGCT 15
Db 1 GCATGACGTGAGCT 15
RESULT 2

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OW nucleic - nucleic search, using sw model

Run on: January 19, 2005, 06:37:10 ; Search time 157.286 Seconds
(without alignments)
547.973 Million cell updates/sec

Title: US-10-789-536-6

Perfect score: 15
Sequence: 1 gcacgacgttgagct 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	9 US-09-824-468-5	Sequence 5, Appl1
2	15	100.0	15	9 US-09-824-468-41	Sequence 41, Appl1
3	15	100.0	15	9 US-09-800-266A-5	Sequence 5, Appl1
4	15	100.0	15	9 US-09-895-007A-5	Sequence 5, Appl1
5	15	100.0	15	9 US-09-920-313-5	Sequence 5, Appl1
6	15	100.0	15	10 US-09-415-142-6	Sequence 6, Appl1
7	15	100.0	15	10 US-09-888-326-65	Sequence 65, Appl1
8	15	100.0	15	10 US-09-888-326-319	Sequence 319, App
9	15	100.0	15	10 US-09-888-326-320	Sequence 320, App
10	15	100.0	15	10 US-09-888-326-321	Sequence 321, App
11	15	100.0	15	10 US-09-888-326-322	Sequence 322, App
12	15	100.0	15	10 US-09-818-918-6	Sequence 6, Appl1

13	15	100.0	15	10 US-09-818-918-16	Sequence 16, Appl1
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16	15	100.0	15	10 US-09-776-479-66	Sequence 66, Appl1
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18	15	100.0	15	10 US-09-776-479-766	Sequence 766, App
19	15	100.0	15	10 US-09-776-479-783	Sequence 783, App
20	15	100.0	15	10 US-09-776-479-835	Sequence 835, App
21	15	100.0	15	10 US-09-954-887B-53	Sequence 53, Appl1
22	15	100.0	15	11 US-09-874-991C-29	Sequence 29, Appl1
23	15	100.0	15	11 US-09-874-991C-95	Sequence 95, Appl1
24	15	100.0	15	11 US-09-874-991C-116	Sequence 116, App
25	15	100.0	15	11 US-09-874-991C-140	Sequence 140, App
26	15	100.0	15	11 US-09-874-991C-167	Sequence 167, App
27	15	100.0	15	11 US-09-874-991C-188	Sequence 188, App
28	15	100.0	15	11 US-09-874-991C-408	Sequence 408, App
29	15	100.0	15	11 US-09-874-991C-427	Sequence 427, App
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33	15	100.0	15	11 US-09-776-479-783	Sequence 783, App
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35	15	100.0	15	13 US-10-023-809A-5	Sequence 5, Appl1
36	15	100.0	15	14 US-10-112-653-60	Sequence 60, Appl1
37	15	100.0	15	14 US-10-112-653-80	Sequence 80, Appl1
38	15	100.0	15	14 US-10-112-653-83	Sequence 83, Appl1
39	15	100.0	15	14 US-10-112-653-739	Sequence 739, App
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41	15	100.0	15	14 US-10-112-653-806	Sequence 806, App
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45	15	100.0	15	14 US-10-017-995-783	Sequence 783, App

ALIGNMENTS

RESULT 1
US-09-824-468-5
Sequence 5, Application US/09824468
Patent No. US20020064515A1
GENERAL INFORMATION:
APPLICANT: Krieger, Arthur M.
APPLICANT: Wehner, George
TITLE OF INVENTION: Methods and Products for Stimulating the
TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
FILE REFERENCE: C1039/7026/HCL
CURRENT APPLICATION NUMBER: US/09/824,468
CURRENT FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 09/286,098
PRIOR FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-824-468-5

Query Match 100.0%; Score 15; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATGACGTGAGCT 15
|||
Db 1 GCATGACGTGAGCT 15

RESULT 2

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 05:49:12 ; Search time 1219.71 Seconds
(without alignments)
448.134 Million cell updates/sec

Title: US-10-789-536-6

Perfect score: 15

Sequence: 1 gcacgacgttcgagct 15

Scoring table:

IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: gb_esc1: *
2: gb_esc2: *
3: gb_hic: *
4: gb_esc3: *
5: gb_esc4: *
6: gb_esc5: *
7: gb_esc6: *
8: gb_gsa1: *
9: gb_gsa2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15	100.0	153	5	BM247469 BM247469
C 2	15	100.0	355	1	AA437702 AA437702
C 3	15	100.0	368	1	AJ494292 AJ494292
C 4	15	100.0	368	1	AJ494293 AJ494293
C 5	15	100.0	376	1	AJ494285 AJ494285
C 6	15	100.0	424	2	BM145624 BM145624
C 7	15	100.0	428	5	BM242018 BM242018
C 8	15	100.0	486	5	BP094747 BP094747
C 9	15	100.0	491	1	AJ495145 AJ495145
C 10	15	100.0	502	1	AV988927 AV988927
C 11	15	100.0	534	1	AV948910 AV948910
C 12	15	100.0	556	1	AV984785 AV984785
C 13	15	100.0	572	1	AV996055 AV996055
C 14	15	100.0	594	1	BM353563 BM353563
C 15	15	100.0	601	1	AV964482 AV964482
C 16	15	100.0	602	5	BM345567 BM345567
C 17	15	100.0	605	5	BM352814 BM352814
C 18	15	100.0	609	5	BM247380 BM247380
C 19	15	100.0	621	5	BM339646 BM339646
C 20	15	100.0	625	5	BM244959 BM244959
C 21	15	100.0	635	1	BM244394 BM244394
C 22	15	100.0	636	1	AV985099 AV985099
C 23	15	100.0	637	5	BU555032 BU555032
C 24	15	100.0	640	5	BM340838 BM340838

C 25	15	100.0	643	5	BM434148 BM434148
C 26	15	100.0	645	1	AV988282 AV988282
C 27	15	100.0	646	5	BM347242 BM347242
C 28	15	100.0	647	1	AV996231 AV996231
C 29	15	100.0	648	5	BM259692 BM259692
C 30	15	100.0	651	1	AV672198 AV672198
C 31	15	100.0	653	5	BM244852 BM244852
C 32	15	100.0	654	1	AV672377 AV672377
C 33	15	100.0	654	5	BM254503 BM254503
C 34	15	100.0	663	5	BU555036 BU555036
C 35	15	100.0	665	5	BM433399 BM433399
C 36	15	100.0	677	5	BM434636 BM434636
C 37	15	100.0	678	1	AV990599 AV990599
C 38	15	100.0	678	6	CA350833 CA350833
C 39	15	100.0	679	5	BM113437 BM113437
C 40	15	100.0	682	5	BM230554 BM230554
C 41	15	100.0	696	1	AV974313 AV974313
C 42	15	100.0	701	5	BM243655 BM243655
C 43	15	100.0	702	5	BM268555 BM268555
C 44	15	100.0	704	5	BM431183 BM431183
C 45	15	100.0	712	5	BM124438 BM124438

ALIGNMENTS

RESULT 1
LOCUS BM247469/c 153 bp mRNA linear EST 09-NOV-2002

DEFINITION BM247469 Nori Satoh unpublished cDNA library, tailbud embryo Clona intestinalis cDNA clone cltb074008 5', mRNA sequence.

ACCESSION BM247469
VERSION BM247469.1 GI:24827387

KEYWORDS EST.

SOURCE Clona intestinalis

ORGANISM Clona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Clonidae; Clona.

REFERENCE 1 (bases 1 to 153)
Sakou, Y., Shin, I.T., Kohara, Y. and Satoh, N.

TITLE Expressed genes in Clona intestinalis (2002c)

JOURNAL Unpublished (2002)

COMMENT Contact: Nori Satoh
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Fax: 81-75-753-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES

Source

1. 153
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="cltb074008"
/tissue_type="whole animal"
/dev_stage="tailbud embryo"
/clone_lib="Nori Satoh unpublished cDNA library, tailbud embryo"

ORIGIN

Query Match 100.0%; Score 15; DB 5; Length 153;
Best Local Similarity 100.0%; Pred. No. 9e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCATGACGTGAGCT 15

Db 62 GCATGACGTGAGCT 48

RESULT 2
LOCUS AA437702/c 355 bp mRNA linear EST 30-MAY-1997